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SEQUENCE LISTING

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Pedersen, Sven
Svendsen, Allan

<120> Fungamyl-like Alpha-Amylase Variants

<130> 5835.200-US

<140> US 09/710,339
<141> 2000-11-09

<150> US 60/165,786
<151> 1999-11-16

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<170> PatentIn version 3.0

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Val Ala Trp Trp Ser Leu Phe Leu Tyr Gly Leu Gln Val Ala Ala Pro
5 10 15

gct ttg gct gca acg cct gcg gac tgg cga tcg caa tcc att tat ttc 152
Ala Leu Ala Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr Phe
20 25 30

ctt ctc acg gat cga ttt gca agg acg gat ggg tcg acg act gcg act 200
Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala Thr
35 40 45

tgt aat act gcg gat cag aaa tac tgt ggt gga aca tgg cag ggc atc 248
Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly Ile
50 55 60 65

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atc gac aag ttg gac tat atc cag gga atg ggc ttc aca gcc atc tgg      296
Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp
                70                  75                  80

atc acc ccc gtt aca gcc cag ctg ccc cag acc acc gca tat gga gat      344
Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly Asp
            85                  90                  95

gcc tac cat ggc tac tgg cag cag gat ata tac tct ctg aac gaa aac      392
Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu Asn
        100                 105                 110

tac ggc act gca gat gac ttg aag gcg ctc tct tcg gcc ctt cat gag      440
Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His Glu
    115                 120                 125

agg ggg atg tat ctt atg gtc gat gtg gtt gct aac cat atg ggc tat      488
Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly Tyr
130                 135                 140                 145

gat gga gcg ggt agc tca gtc gat tac agt gtg ttt aaa ccg ttc agt      536
Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe Ser
                150                 155                 160

tcc caa gac tac ttc cac ccg ttc tgt ttc att caa aac tat gaa gat      584
Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu Asp
            165                 170                 175

cag act cag gtt gag gat tgc tgg cta gga gat aac act gtc tcc ttg      632
Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser Leu
        180                 185                 190

cct gat ctc gat acc acc aag gat gtg gtc aag aat gaa tgg tac gac      680
Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr Asp
    195                 200                 205

tgg gtg gga tca ttg gta tcg aac tac tcc att gac ggc ctc cgt atc      728
Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg Ile
210                 215                 220                 225

gac aca gta aaa cac gtc cag aag gac ttc tgg ccc ggg tac aac aaa      776
Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn Lys
                230                 235                 240

gcc gca ggc gtg tac tgt atc ggc gag gtg ctc gac ggt gat ccg gcc      824
Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro Ala
            245                 250                 255

tac act tgt ccc tac cag aac gtc atg gac ggc gta ctg aac tat ccc      872
Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr Pro
        260                 265                 270
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B' cont.

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att tac tat cca ctc ctc aac gcc ttc aag tca acc tcc ggc agc atg      920
Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser Met
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gac gac ctc tac aac atg atc aac acc gtc aaa tcc gac tgt cca gac      968
Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro Asp
290                 295                 300                 305

tca aca ctc ctg ggc aca ttc gtc gag aac cac gac aac cca cgg ttc     1016
Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg Phe
                310                 315                 320

gct tct tac acc aac gac ata gcc ctc gcc aag aac gtc gca gca ttc     1064
Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala Phe
            325                 330                 335

atc atc ctc aac gac gga atc ccc atc atc tac gcc ggc caa gaa cag     1112
Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu Gln
        340                 345                 350

cac tac gcc ggc gga aac gac ccc gcg aac cgc gaa gca acc tgg ctc     1160
His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp Leu
    355                 360                 365

tcg ggc tac ccg acc gac agc gag ctg tac aag tta att gcc tcc gcg     1208
Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser Ala
370                 375                 380                 385

aac gca atc cgg aac tat gcc att agc aaa gat aca gga ttc gtg acc     1256
Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val Thr
                390                 395                 400

tac aag aac tgg ccc atc tac aaa gac gac aca acg atc gcc atg cgc     1304
Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met Arg
            405                 410                 415

aag ggc aca gat ggg tcg cag atc gtg act atc ttg tcc aac aag ggt     1352
Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys Gly
        420                 425                 430

gct tcg ggt gat tcg tat acc ctc tcc ttg agt ggt gcg ggt tac aca     1400
Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr Thr
    435                 440                 445

gcc ggc cag caa ttg acg gag gtc att ggc tgc acg acc gtg acg gtt     1448
Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr Val
450                 455                 460                 465

ggt tcg gat gga aat gtg cct gtt cct atg gca ggt ggg cta cct agg     1496
Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro Arg
                470                 475                 480
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B' cont.

gta ttg tat ccg act gag aag ttg gca ggt agc aag atc tgt agt agc 1544
Val Leu Tyr Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser Ser
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tcg tgaagggtgg agagtatatg atggtactgc tattcaatct ggcattggac 1597
Ser

agtgagtttg agtttgatgt acagttggag tcgttactgc tgtcatcccc ttatactctt 1657

cgattgtttt tcgaacccta atgccaagca cgctagtcta ttataggaaa aaaaaaaaaa 1717

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<212> PRT
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Pro Ala Leu Ala Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr
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Phe Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala
35 40 45

Thr Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly
50 55 60

Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile
65 70 75 80

Trp Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly
85 90 95

Asp Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu
100 105 110

Asn Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His
115 120 125

Glu Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly
130 135 140

Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe
145 150 155 160

Ser Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu
165 170 175

Asp Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser
180 185 190

Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr
195 200 205

B' cont.

Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg
210 215 220

Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn
225 230 235 240

Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro
245 250 255

Ala Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr
260 265 270

Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser
275 280 285

Met Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro
290 295 300

Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg
305 310 315 320

Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala
325 330 335

Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu
340 345 350

Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp
355 360 365

Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser
370 375 380

Ala Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val
385 390 395 400

Thr Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met
405 410 415

B' cont.

Arg Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys
420 425 430

Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr
435 440 445

Thr Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr
450 455 460

Val Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro
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Ser Ser

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Phe Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala
        35                  40                  45

Thr Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly
    50                  55                  60

Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile
65                  70                  75                  80

Trp Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly
                85                  90                  95

Asp Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu
            100                 105                 110

Asn Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His
        115                 120                 125

Glu Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly
    130                 135                 140

Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe
145                 150                 155                 160

Ser Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu
                165                 170                 175

Asp Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser
            180                 185                 190

Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr
        195                 200                 205

Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg
    210                 215                 220

Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn
225                 230                 235                 240

Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro
                245                 250                 255

Ala Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr
            260                 265                 270
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B' cont.

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Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser
        275                 280                 285

Met Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro
    290                 295                 300

Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg
305                 310                 315                 320

Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala
                325                 330                 335

Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu
            340                 345                 350

Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp
        355                 360                 365

Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser
    370                 375                 380

Ala Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val
385                 390                 395                 400

Thr Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met
                405                 410                 415

Arg Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys
            420                 425                 430

Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr
        435                 440                 445

Thr Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr
    450                 455                 460

Val Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro
465                 470                 475                 480

Arg Val Leu Tyr Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser
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Ser Ser
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B' cont.

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<210> 5
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<213> artificial

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<400> 5
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B' cont.